Fig. 1

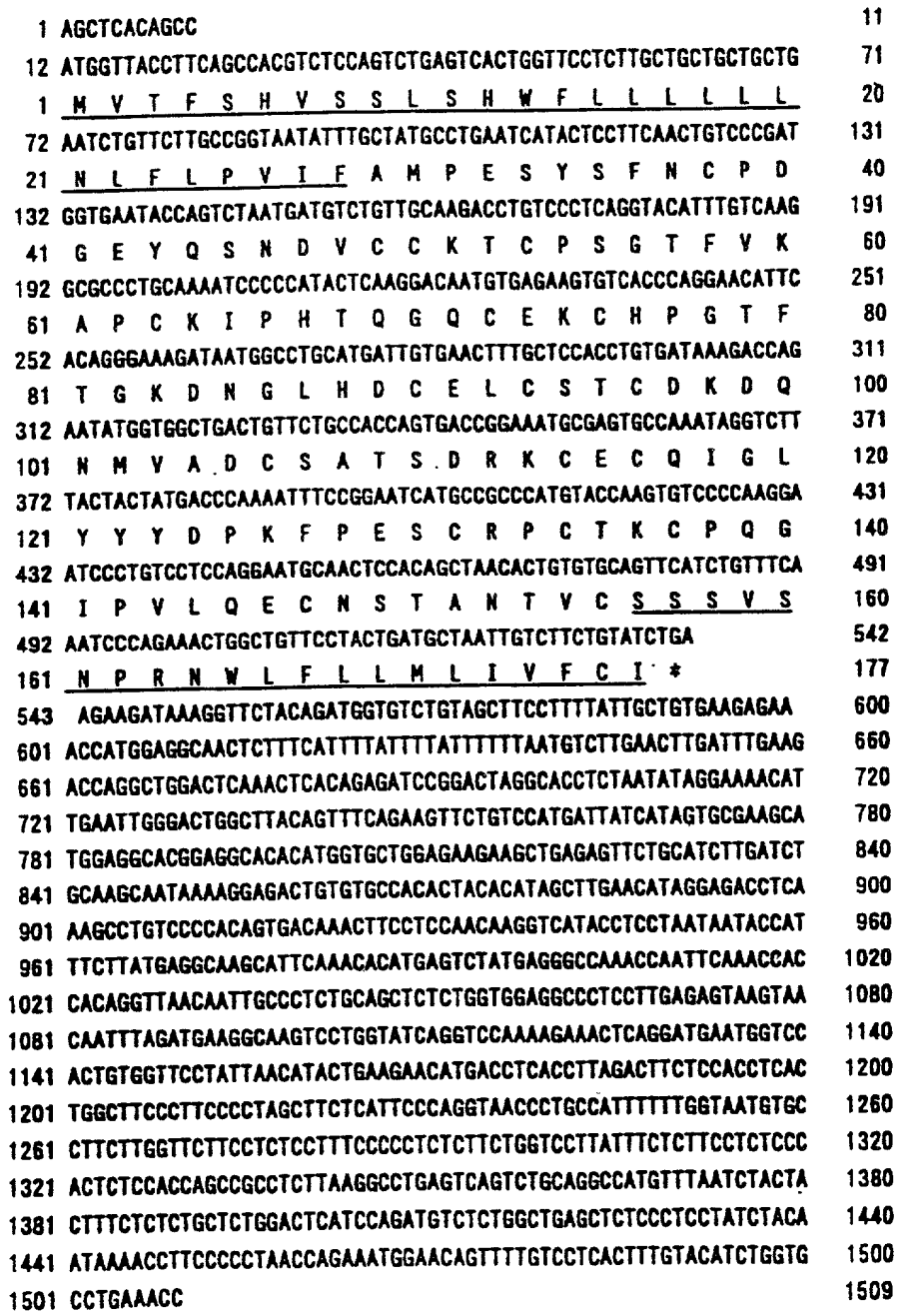

1 AGCTCACAGCC 11
12 ATGGTTACCTTCAGCCACGTCTCCAGTCTGAGTCACTGGTTCCTCTTGCTGCTGCTGCTG 71
1 M V T F S H V S S L S H W F L L L L L L 20
72 AATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATCATACTCCTTCAACTGTCCCGAT 131
21 N L F L P V I F A M P E S Y S F N C P D 40
132 GGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTGTCCCTCAGGTACATTTGTCAAG 191
41 G E Y Q S N D V C C K T C P S G T F V K 60
192 GCGCCCTGCAAAATCCCCCATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTC 251
61 A P C K I P H T Q G Q C E K C H P G T F 80
252 ACAGGGAAAGATAATGGCCTGCATGATTGTGAACTTTGCTCCACCTGTGATAAAGACCAG 311
81 T G K D N G L H D C E L C S T C D K D Q 100
312 AATATGGTGGCTGACTGTTCTGCCACCAGTGACCGGAAATGCGAGTGCCAAATAGGTCTT 371
101 N M V A D C S A T S D R K C E C Q I G L 120
372 TACTACTATGACCCAAAATTTCCGGAATCATGCCGCCCATGTACCAAGTGTCCCCAAGGA 431
121 Y Y Y D P K F P E S C R P C T K C P Q G 140
432 ATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCA 491
141 I P V L Q E C N S T A N T V C S S S V S 160
492 AATCCCAGAAACTGGCTGTTCCTACTGATGCTAATTGTCTTCTGTATCTGA 542
161 N P R N W L F L L M L I V F C I * 177
543 AGAAGATAAAGGTTCTACAGATGGTGTCTGTAGCTTCCTTTTATTGCTGTGAAGAGAA 600
601 ACCATGGAGGCAACTCTTTCATTTTATTTTATTTTTTAATGTCTTGAACTTGATTTGAAG 660
661 ACCAGGCTGGACTCAAACTCACAGAGATCCGGACTAGGCACCTCTAATATAGGAAAACAT 720
721 TGAATTGGGACTGGCTTACAGTTTCAGAAGTTCTGTCCATGATTATCATAGTGCGAAGCA 780
781 TGGAGGCACGGAGGCACACATGGTGCTGGAGAAGAAGCTGAGAGTTCTGCATCTTGATCT 840
841 GCAAGCAATAAAAGGAGACTGTGTGCCACACTACACATAGCTTGAACATAGGAGACCTCA 900
901 AAGCCTGTCCCCACAGTGACAAACTTCCTCCAACAAGGTCATACCTCCTAATAATACCAT 960
961 TTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAC 1020
1021 CACAGGTTAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCCTTGAGAGTAAGTAA 1080
1081 CAATTTAGATGAAGGCAAGTCCTGGTATCAGGTCCAAAAGAAACTCAGGATGAATGGTCC 1140
1141 ACTGTGGTTCCTATTAACATACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCAC 1200
1201 TGGCTTCCCTTCCCCTAGCTTCTCATTCCCAGGTAACCCTGCCATTTTTTGGTAATGTGC 1260
1261 CTTCTTGGTTCTTCCTCTCCTTTCCCCCTCTCTTCTGGTCCTTATTTCTCTTCCTCTCCC 1320
1321 ACTCTCCACCAGCCGCCTCTTAAGGCCTGAGTCAGTCTGCAGGCCATGTTTAATCTACTA 1380
1381 CTTTCTCTCTGCTCTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCCTATCTACA 1440
1441 ATAAAACCTTCCCCCTAACCAGAAATGGAACAGTTTTGTCCTCACTTTGTACATCTGGTG 1500
1501 CCTGAAACC 1509

Fig. 2

```
7F4    CPDGEY---QSNDVC CKTCPSGTFVKAPCK IPHTQGQCEKCHPGT FTGKDNGLHDCELCS 60
mTNFR CPGGKYVHSKNNSIC CTKCHKGTYLVSDCP SPGRDTVCRECEKGT FTASQNYLRQCLSCK 60

7F4    TCDKD--QNMVADCS ATSDRKCEC---QIG LYYYDPKFPESCRPC TKCPQGIPVLQECNS 120
mTNFR TCRKEMSQVEISPCQ ADKDTVCGCKENQFQ RYLSETHFQ--CVDC SPCFNGTVTIP-CKE 120

7F4    TANTVC                                                          126
mTNFR TQNTVC                                                          126
```

Fig. 3

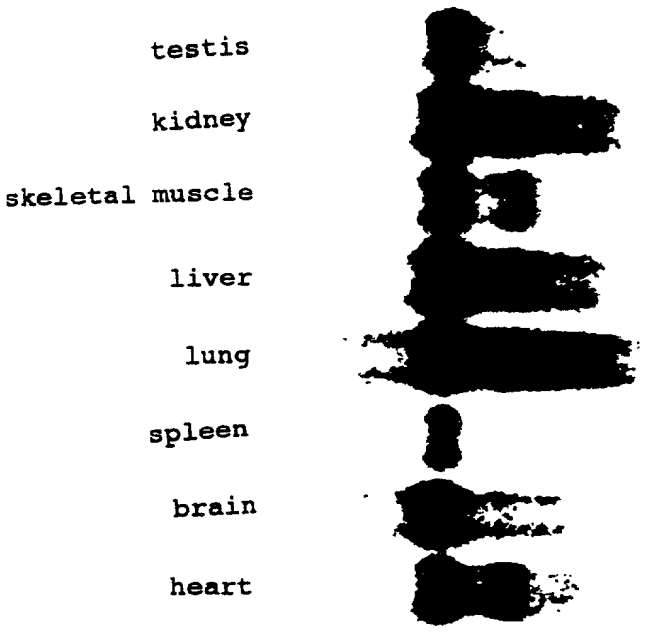

testis
kidney
skeletal muscle
liver
lung
spleen
brain
heart

Fig. 4

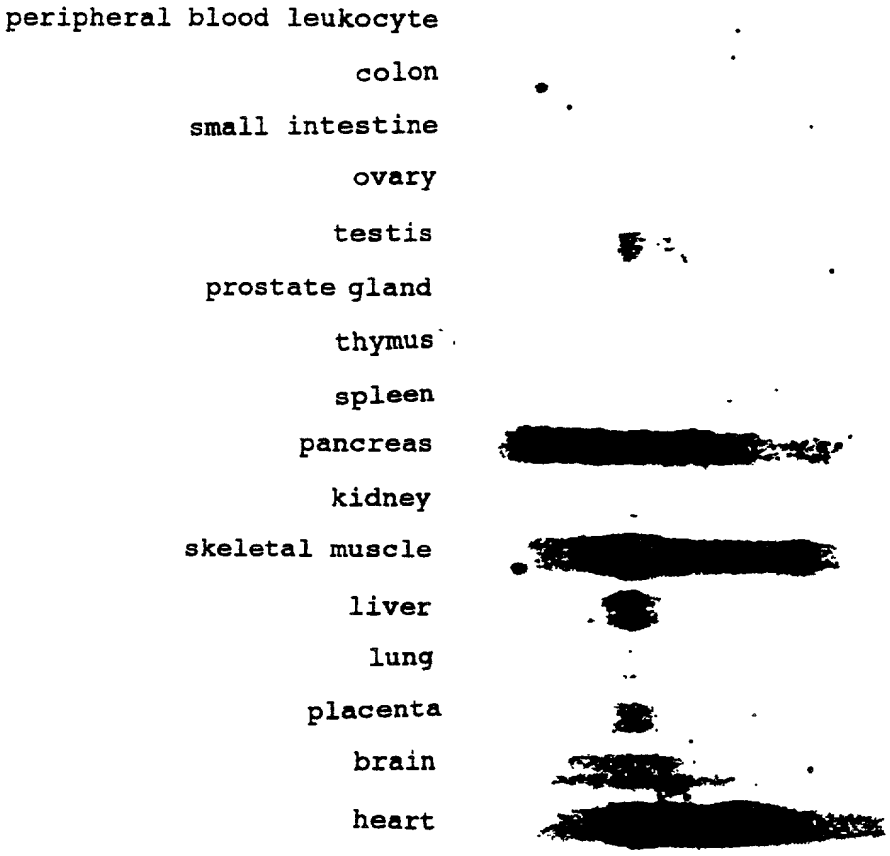

peripheral blood leukocyte
colon
small intestine
ovary
testis
prostate gland
thymus
spleen
pancreas
kidney
skeletal muscle
liver
lung
placenta
brain
heart

Fig. 5A

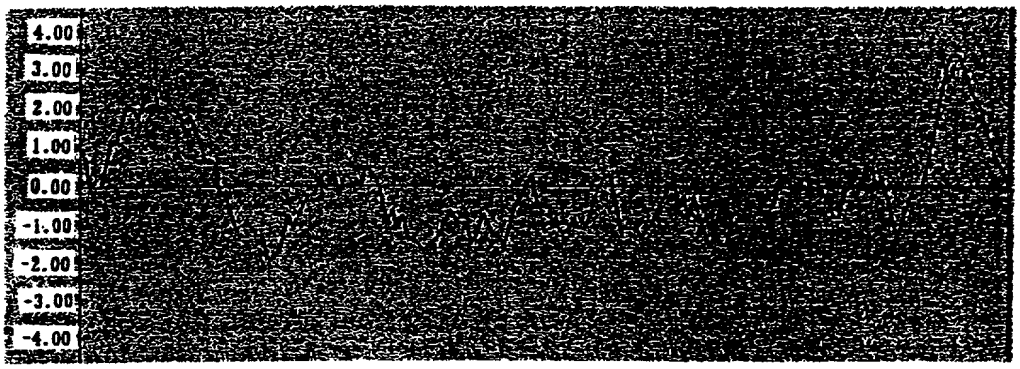

4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00

Fig. 5B

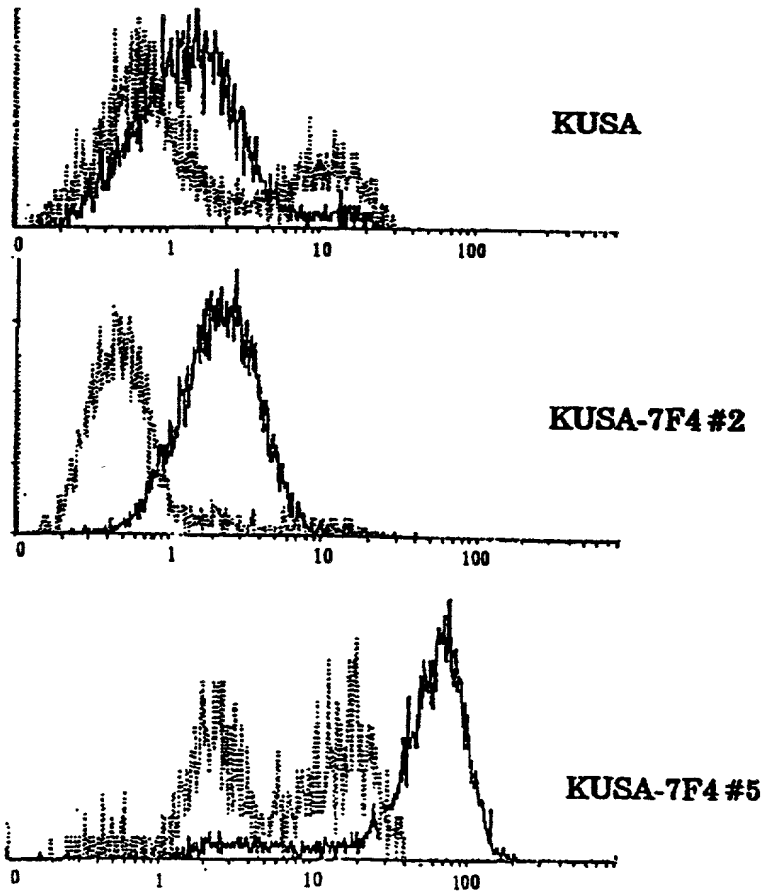

KUSA
0
1
10
100
KUSA-7F4 #2
0
1
10
100
KUSA-7F4 #5
0
1
10
100

Fig. 6

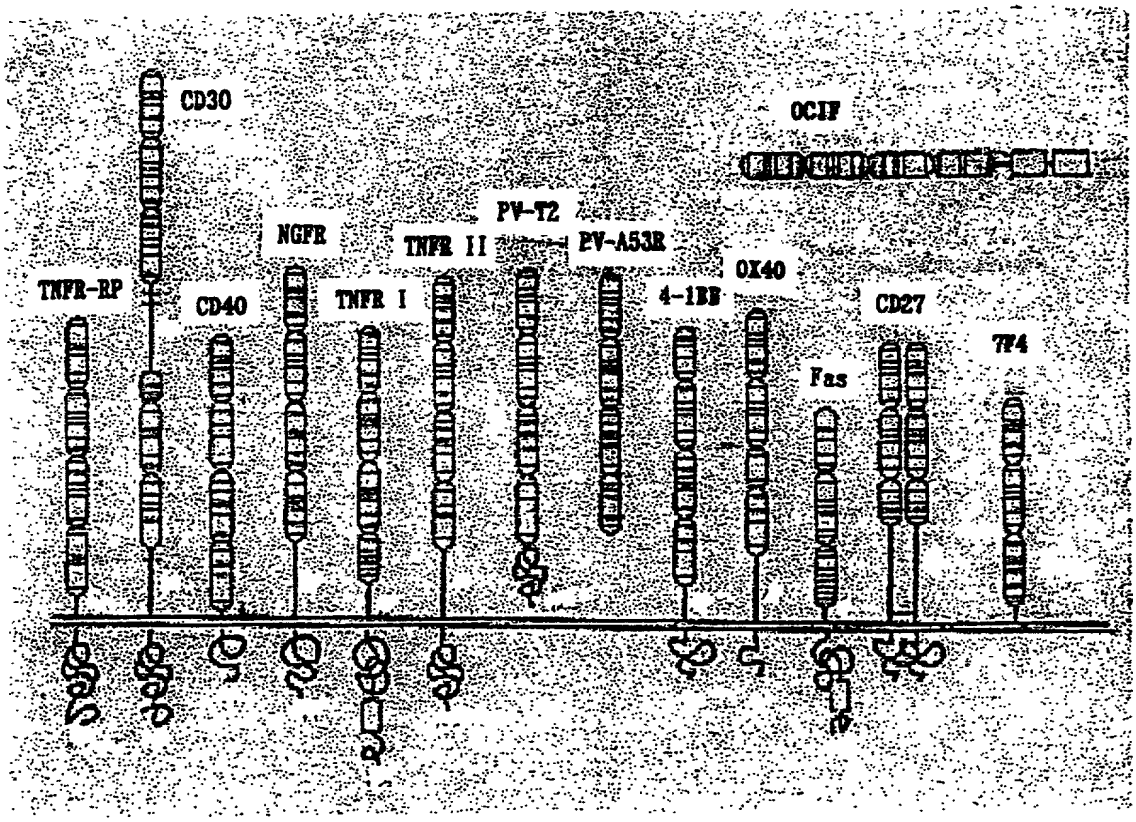

CD30
OCIF
PV-T2
NGFR
TNFR II
PV-A53R
TNFR-RP
CD40
TNFR I
4-1BB
OX40
CD27
Fas
TP4

Fig. 7

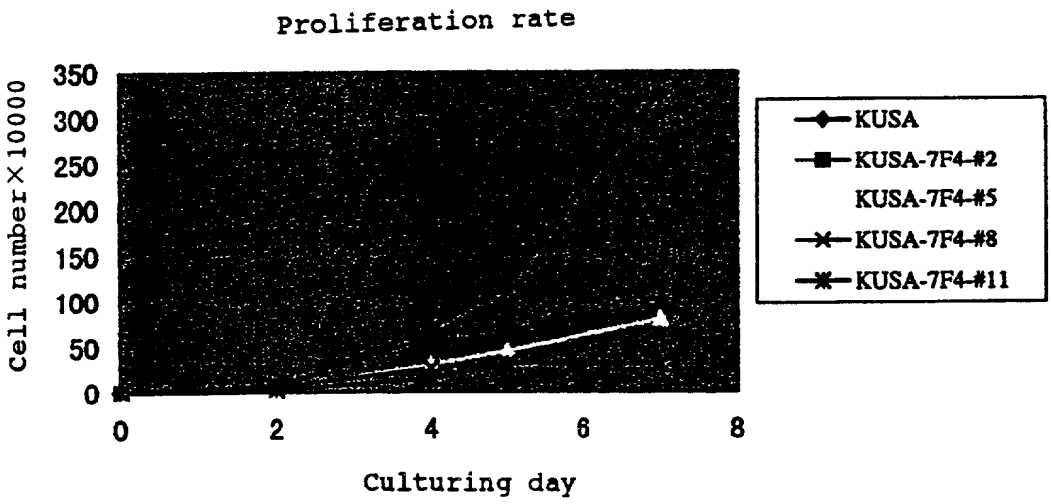

Proliferation rate
Cell number×10000
350
300
250
200
150
100
50
0
0
2
4
6
8
Culturing day
KUSA
KUSA-7F4-#2
KUSA-7F4-#5
KUSA-7F4-#8
KUSA-7F4-#11

Fig. 8

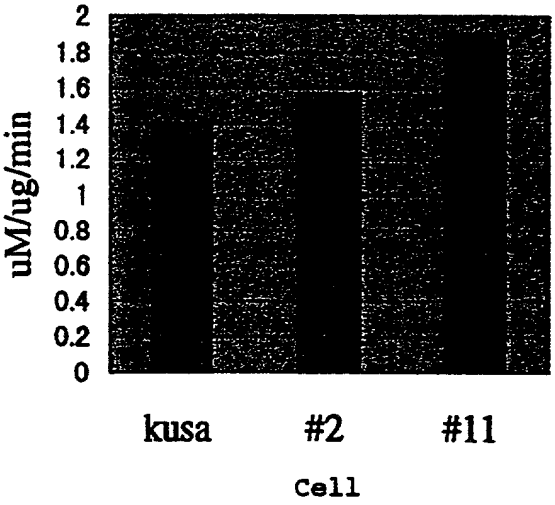


Fig. 9

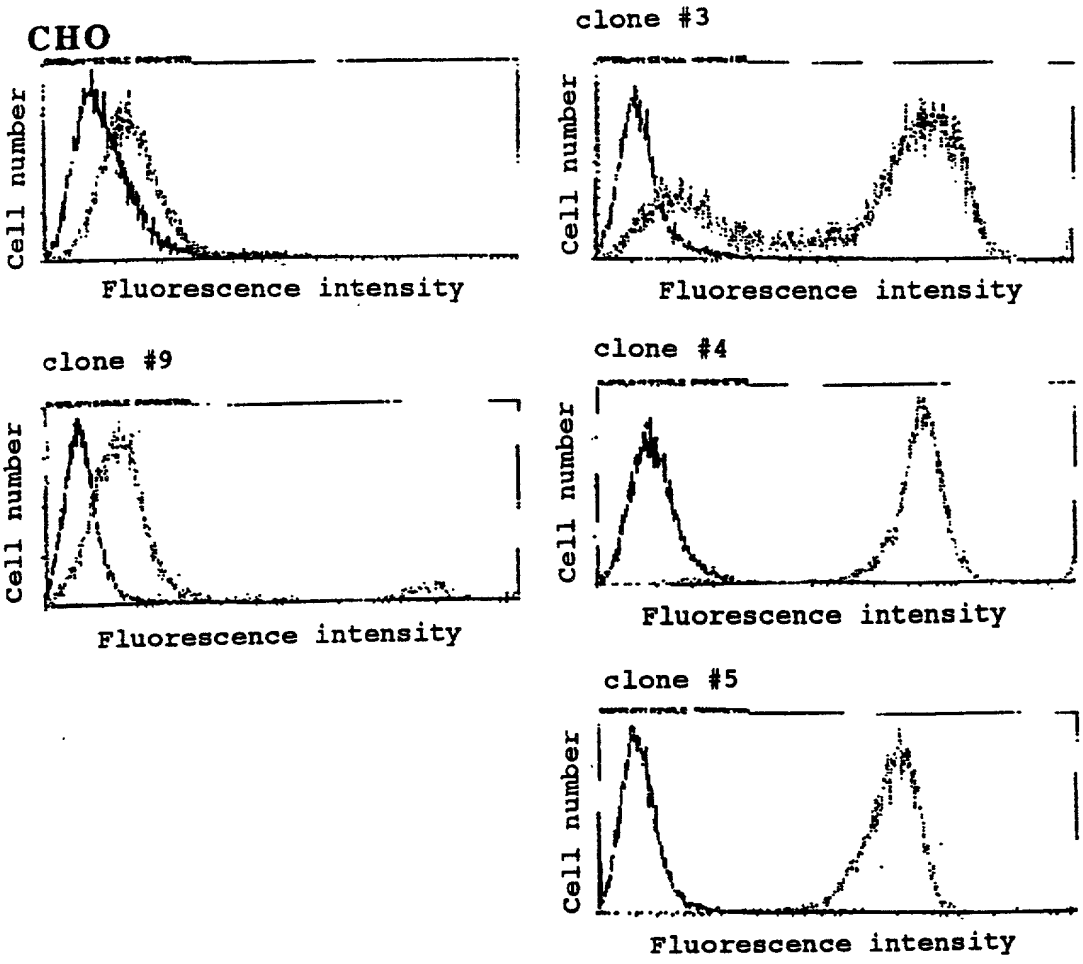
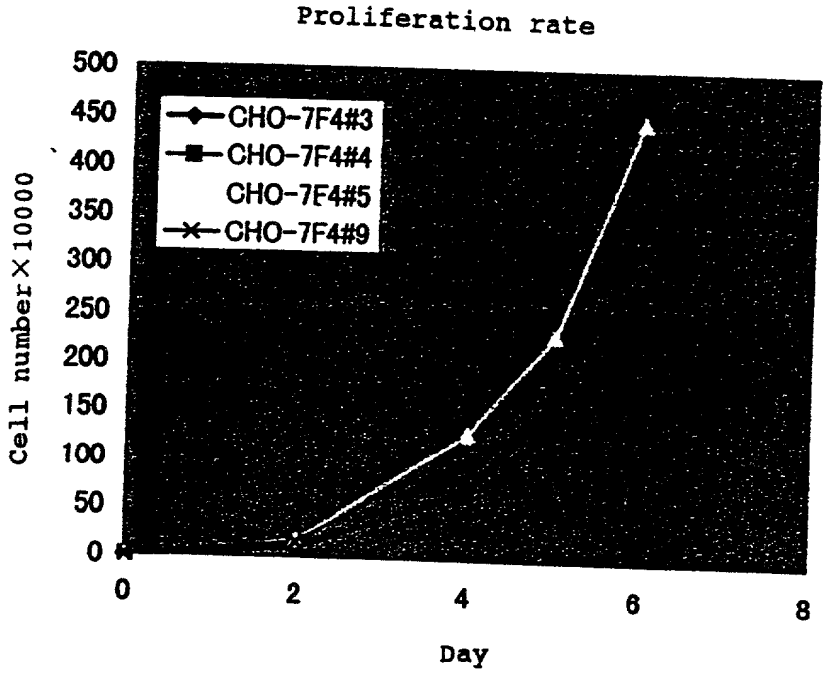

CHO
Cell number
Fluorescence intensity
clone #3
Cell number
Fluorescence intensity
clone #9
Cell number
Fluorescence intensity
clone #4
Cell number
Fluorescence intensity
clone #5
Cell number
Fluorescence intensity

Fig. 10


Proliferation rate
Cell number×10000
500
450
400
350
300
250
200
150
100
50
0
0
2
4
6
8
Day
CHO-7F4#3
CHO-7F4#4
CHO-7F4#5
CHO-7F4#9